

SEQUENCE LISTING

<110> FARWICK, Mike

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BATHE, Brigitte

<120> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE RODA PROTEIN

<130> 212532US0

<150> DE10044943.3

<151> 2000-09-12

<150> DE10132947.4

<151> 2001-07-06

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 1761

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (238) .. (1560)

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cgaggtccag gcgcaaattgc aacgggtggc tgctcaagct ttgccagtgt gcgtgaactt 180  
agaagtaaca accgggtggcg atagaaacga acccggagtc aattgtaggg aggtctc 237  
atg aac acg ctt gaa cga tta aag ctt cgt cgc acg gaa atg tgg ctg 285  
Met Asn Thr Leu Glu Arg Leu Lys Leu Arg Arg Thr Glu Met Trp Leu  
5 10 15  
ctg ata ctt gcc aca ctc gtt gtg tcg atc atg ttc atc agc ctc gag 333  
Leu Ile Leu Ala Thr Leu Val Val Ser Ile Met Phe Ile Ser Leu Glu  
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Leu Ala Met Gly Asn Glu Leu Gly Thr His Ile Leu Met Leu Met Gly  
35 40 45  
aga tat atc ggt atc ttc atc gtc gcg cac cta gcc atg gca tgg gtg 429  
Gly Tyr Ile Gly Ile Phe Ile Val Ala His Leu Ala Met Ala Trp Val  
50 55 60  
gcg ccg ttt gct gat caa atc atg ctg cct gtg gtg gcg gtg ctc aat 477  
Ala Pro Phe Ala Asp Gln Ile Met Leu Pro Val Val Ala Val Leu Asn  
65 70 75 80  
ggc att ggt ttg gtg atg att tat cgc ctt gat gag gcc acg ggc tac 525  
Gly Ile Gly Leu Val Met Ile Tyr Arg Leu Asp Glu Ala Thr Gly Tyr  
85 90 95  
agc acg gtc aat agc caa ttg atg tgg acg gtt gtt ggc gtc acg ctg 573  
Ser Thr Val Asn Ser Gln Leu Met Trp Thr Val Val Gly Val Thr Leu  
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atg gtg gct gtg ttg ttg ctg ttg cgt gat tac aag tcg ctt tcg cgt 621  
Met Val Ala Val Leu Leu Leu Leu Arg Asp Tyr Lys Ser Leu Ser Arg  
115 120 125  
tat tcc tac ctc ctc ggt gtg gtg ggc atc gtg ctg ctg gcg ctg cct 669  
Tyr Ser Tyr Leu Leu Gly Val Val Gly Ile Val Leu Leu Ala Leu Pro  
130 135 140

ctc	gtg	tgg	ccg	cag	cca	ggc	ggc	gtg	gaa	gcc	cgc	atc	tgg	att	tgg	717
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Leu	Gly	Pro	Phe	Ser	Ile	Gln	Pro	Gly	Glu	Phe	Ser	Lys	Ile	Leu	Leu	
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Leu	Leu	Phe	Phe	Ala	Gln	Leu	Leu	Ala	Thr	Lys	Arg	Ala	Leu	Phe	Thr	
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Val	Ala	Gly	Tyr	Arg	Phe	Leu	Gly	Met	Asp	Phe	Pro	Arg	Leu	Arg	Asp	
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cct	gtc	gtg	cac	tcg	gac	ttc	att	ctc	gca	gcc	att	ggc	gag	gag	ctt	1245
Pro	Val	Val	His	Ser	Asp	Phe	Ile	Leu	Ala	Ala	Ile	Gly	Glu	Glu	Leu	
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 Thr Arg Gly Met Arg Thr Ala Thr Leu Ala Arg Asp Ser Tyr Gly Lys  
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gtc gtg gca ggt att tct tca ctg atg ccc atg aca ggt ttg acc act 1437  
 Val Val Ala Gly Ile Ser Ser Leu Met Pro Met Thr Gly Leu Thr Thr  
 385 390 395 400

ccg ttt atg tcc cag ggt ggt tca tcc ctg atg gct aac tac att ctg 1485  
 Pro Phe Met Ser Gln Gly Gly Ser Ser Leu Met Ala Asn Tyr Ile Leu  
 405 410 415

atg gcc atc atc ttg cgt att tct gac agt gcc cgc cga cct gtc atg 1533  
 Met Ala Ile Ile Leu Arg Ile Ser Asp Ser Ala Arg Arg Pro Val Met  
 420 425 430

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gcttttaggg acgatgatct tgctcagaac ccactgaacg cacgtgggtt cctggaggcg 1700

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<211> 441

<212> PRT

<213> Corynebacterium glutamicum

<400> 2

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Leu Ala Met Gly Asn Glu Leu Gly Thr His Ile Leu Met Leu Met Gly  
35 40 45

Gly Tyr Ile Gly Ile Phe Ile Val Ala His Leu Ala Met Ala Trp Val  
50 55 60

Ala Pro Phe Ala Asp Gln Ile Met Leu Pro Val Val Ala Val Leu Asn  
65 70 75 80

Gly Ile Gly Leu Val Met Ile Tyr Arg Leu Asp Glu Ala Thr Gly Tyr  
85 90 95

Ser Thr Val Asn Ser Gln Leu Met Trp Thr Val Val Gly Val Thr Leu  
100 105 110

Met Val Ala Val Leu Leu Leu Leu Arg Asp Tyr Lys Ser Leu Ser Arg  
115 120 125

Tyr Ser Tyr Leu Leu Gly Val Val Gly Ile Val Leu Leu Ala Leu Pro  
130 135 140

Leu Val Trp Pro Gln Pro Gly Gly Val Glu Ala Arg Ile Trp Ile Trp  
145 150 155 160

Leu Gly Pro Phe Ser Ile Gln Pro Gly Glu Phe Ser Lys Ile Leu Leu  
165 170 175

Leu Leu Phe Phe Ala Gln Leu Leu Ala Thr Lys Arg Ala Leu Phe Thr  
180 185 190

Val Ala Gly Tyr Arg Phe Leu Gly Met Asp Phe Pro Arg Leu Arg Asp  
195 200 205

Leu Ala Pro Ile Leu Val Val Trp Ala Leu Ala Ile Leu Ile Met Ala  
210 215 220

Gly Ala Asn Asp Phe Gly Pro Ala Leu Leu Leu Phe Thr Thr Val Leu  
225 230 235 240

Ala Met Val Tyr Leu Ala Thr Gly Arg Gly Ser Trp Leu Leu Ile Gly  
245 250 255

Ala Val Leu Val Ala Val Gly Ala Phe Ala Val Tyr Gln Val Ser Ser  
260 265 270

Lys Ile Gln Glu Arg Val Gln Asn Phe Val Asp Pro Val Ala His Tyr  
275 280 285

Asp Thr Thr Gly Tyr Gln Leu Ser Gln Ser Leu Phe Gly Met Ser Trp  
290 295 300

Gly Gly Ile Thr Gly Thr Gly Ile Gly Gln Gly Tyr Pro Asn Met Ile  
305 310 315 320

Pro Val Val His Ser Asp Phe Ile Leu Ala Ala Ile Gly Glu Glu Leu  
325 330 335

Gly Leu Ile Gly Leu Ala Ala Ile Ile Val Leu Phe Gly Val Phe Val  
340 345 350

Thr Arg Gly Met Arg Thr Ala Thr Leu Ala Arg Asp Ser Tyr Gly Lys  
355 360 365

Leu Val Ala Ser Gly Leu Ser Met Thr Ile Met Ile Gln Ile Phe Val  
370 375 380

Val Val Ala Gly Ile Ser Ser Leu Met Pro Met Thr Gly Leu Thr Thr  
385 390 395 400

Pro Phe Met Ser Gln Gly Gly Ser Ser Leu Met Ala Asn Tyr Ile Leu  
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Met Ala Ile Ile Leu Arg Ile Ser Asp Ser Ala Arg Arg Pro Val Met  
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Ser Lys Gln Ala Ser Glu Val Ala Ala  
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<213> Artificial Sequence

<223> synthetic DNA

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213> Artificial Sequence

~~223~~ synthetic DNA

ctctgcagga gggatgtgat tcgaatcg

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